

“Complete Plastome and Molecular Phylogeny of Gracilaria Seaweeds (Rhodophyta : Gracilariaceae)”

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In this study, the chloroplast genome of *G. changii* and *G. salicornia* from peninsular Malaysia were sequenced to compare with the published taxa in order to gain a better understanding of the phylogenetic questions that remain for the red algae, particularly *G. changii* and *G. firma*. Phylogenetic analysis using 77 recommended protein-coding genes showed that *G. changii* formed a sister lineage with *G. firma* with genetic distance of 0.43%, and *G. changii* of this study was conspecific with *G. changii* in GenBank with genetic distance of 0%. A similar condition of small genetic distance was found in *G. salicornia* from peninsular Malaysia and Hawaii with $p = 0.06\%$. Five potential chloroplast genes (*petF*, *rps12*, *rps14*, *rp18* and *petB*) showed higher variation of genetic distance between *G. changii* and *G. firma* ($p = 1.23\text{--}2.00\%$) and that between peninsular Malaysia and Hawaii *G. salicornia* from $p = 0\text{--}0.30\%$. Other genes (*cox1* and *rbcL*) also indicate that *G. changii* and *G. firma* are genetically distinct. It is evident that multi-gene analysis and extensive taxon sampling, particularly from type locality, will present a better phylogeny.

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